

Sequence listing

<110> SHANGHAI CANCER INSTITUTE

<120> A HUMAN TUMOR-ASSOCIATED GENE CT120 ON CHROMOSOME 17P 13.3 REGION AND PROTEIN ENCODED BY IT

<130> 024832pc

<150> CN 02150730.9

<151> 2002-11-27

<160> 13

<170> PatentIn version 3.1

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<211> 2145

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (91).. (861)

<223>

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Met Leu Leu Thr Leu Ala Gly Gly	
1 5	
gcg ctc ttc ttc ccg ggg ctc ttc gcg ctc tgc acc tgg gcg ctg cgc	162
Ala Leu Phe Phe Pro Gly Leu Phe Ala Leu Cys Thr Trp Ala Leu Arg	
10 15 20	
cac tcc cag ccc gga tgg agc cgc acc gac tgc gtg atg atc agc acc	210
His Ser Gln Pro Gly Trp Ser Arg Thr Asp Cys Val Met Ile Ser Thr	
25 30 35 40	
agg ctg gtt tcc tcg gtg cac gcc gtg ctg gcc acc ggc tcg ggg atc	258
Arg Leu Val Ser Ser Val His Ala Val Leu Ala Thr Gly Ser Gly Ile	
45 50 55	
gtc atc att cgc tcc tgc gac gac gtg atc acc ggc agg cac tgg ctt	306
Val Ile Ile Arg Ser Cys Asp Asp Val Ile Thr Gly Arg His Trp Leu	
60 65 70	
gcc cgg gaa tat gtg tgg ttt ctg att cca tac atg atc tat gac tcg	354
Ala Arg Glu Tyr Val Trp Phe Leu Ile Pro Tyr Met Ile Tyr Asp Ser	
75 80 85	
tac gcc atg tac ctc tgt gaa tgg tgc cga acc aga gac cag aac cgt	402
Tyr Ala Met Tyr Leu Cys Glu Trp Cys Arg Thr Arg Asp Gln Asn Arg	
90 95 100	
gcg ccc tcc ctc act ctt cga aac ttc cta agt cga aac cgc ctc atg	450
Ala Pro Ser Leu Thr Leu Arg Asn Phe Leu Ser Arg Asn Arg Leu Met	
105 110 115 120	
atc aca cat cat gcg gtc att ctc ctt gtc ctt gtg cca gtc gca cag	498
Ile Thr His His Ala Val Ile Leu Leu Val Leu Val Pro Val Ala Gln	
125 130 135	
agg ctc cgg gga gac ctt ggg gac ttc ttt gtc ggc tgc atc ttc acg	546
Arg Leu Arg Gly Asp Leu Gly Asp Phe Phe Val Gly Cys Ile Phe Thr	
140 145 150	
gca gaa ctg agc act ccg ttt gtg tcg ctg ggc agg gtt ctg att cag	594
Ala Glu Leu Ser Thr Pro Phe Val Ser Leu Gly Arg Val Leu Ile Gln	

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cta aag cag cag cac acc ctt ctg tac aag gtg aat gga atc ctc acg      642
Leu Lys Gln Gln His Thr Leu Leu Tyr Lys Val Asn Gly Ile Leu Thr
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ctg gcc acc ttc ctt tcc tgc cgg atc ctt ctc ttc ccc ttc atg tac      690
Leu Ala Thr Phe Leu Ser Cys Arg Ile Leu Leu Phe Pro Phe Met Tyr
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tgg tcc tat ggc cgc cag cag gga cta agc ctg ctc caa gta ccc ttc      738
Trp Ser Tyr Gly Arg Gln Gln Gly Leu Ser Leu Leu Gln Val Pro Phe
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agc atc cca ttc tac tgc aac gtg gcc aat gcc ttc ctc gta gct cct      786
Ser Ile Pro Phe Tyr Cys Asn Val Ala Asn Ala Phe Leu Val Ala Pro
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cag atc tac tgg ttc tgt ctg ctg tgc agg aag gca gtc cgg ctc ttt      834
Gln Ile Tyr Trp Phe Cys Leu Leu Cys Arg Lys Ala Val Arg Leu Phe
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gac act ccc caa gcc aaa aag gat ggc taaatgctcc tgggagtcag      881
Asp Thr Pro Gln Ala Lys Lys Asp Gly
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Thr Asp Cys Val Met Ile Ser Thr Arg Leu Val Ser Ser Val His Ala
35      40      45
Val Leu Ala Thr Gly Ser Gly Ile Val Ile Ile Arg Ser Cys Asp Asp
50      55      60
Val Ile Thr Gly Arg His Trp Leu Ala Arg Glu Tyr Val Trp Phe Leu
65      70      75      80
Ile Pro Tyr Met Ile Tyr Asp Ser Tyr Ala Met Tyr Leu Cys Glu Trp
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Cys Arg Thr Arg Asp Gln Asn Arg Ala Pro Ser Leu Thr Leu Arg Asn
100      105      110
Phe Leu Ser Arg Asn Arg Leu Met Ile Thr His His Ala Val Ile Leu

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115 120 125
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 130 135 140
 Phe Phe Val Gly Cys Ile Phe Thr Ala Glu Leu Ser Thr Pro Phe Val
 145 150 155 160
 Ser Leu Gly Arg Val Leu Ile Gln Leu Lys Gln Gln His Thr Leu Leu
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 Tyr Lys Val Asn Gly Ile Leu Thr Leu Ala Thr Phe Leu Ser Cys Arg
 180 185 190
 Ile Leu Leu Phe Pro Phe Met Tyr Trp Ser Tyr Gly Arg Gln Gln Gly
 195 200 205
 Leu Ser Leu Leu Gln Val Pro Phe Ser Ile Pro Phe Tyr Cys Asn Val
 210 215 220
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 245 250 255
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<400> 11

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